

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 12:29:37 ; Search time 73 Seconds
(without alignments)
535.637 Million cell updates/sec

Title: US-10-063-728-114

Perfect score: 595
Sequence: 1 MIMWLVLILLPTLKSVFCSL.....ABPLGSCGFQGGPCRRRD 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:**

- 1: geneseqp1980s:**
- 2: geneseqp1990s:**
- 3: geneseqp2000s:**
- 4: geneseqp2001s:**
- 5: geneseqp2002s:**
- 6: geneseqp2003as:**
- 7: geneseqp2003bs:**
- 8: geneseqp2004s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	100.0	109	3	AAV94964 Human sec
2	595	100.0	109	3	AAV87344 Human sig
3	595	100.0	109	3	AAV99424 Human PRO
4	595	100.0	109	4	AAV66173 Protein o
5	595	100.0	109	4	AAU29195 Human PRO
6	595	100.0	109	4	AAV87582 Human PRO
7	595	100.0	109	5	ABG95907 Human sec
8	595	100.0	109	6	ABU85571 Human PRO
9	595	100.0	109	6	ABU88119 Novel hum
10	595	100.0	109	6	ABU84434 Human sec
11	595	100.0	109	6	ABR65308 Human sec
12	595	100.0	109	6	ABR65638 Human sec
13	595	100.0	109	6	ABU99638 Human sec
14	595	100.0	109	6	ABU82877 Human PRO
15	595	100.0	109	6	ABU89998 Novel hum
16	595	100.0	109	6	ABR68247 Human sec
17	595	100.0	109	6	ABU96300 Novel hum
18	595	100.0	109	6	ABU92731 Human sec
19	595	100.0	109	6	ABO08808 Human sec
20	595	100.0	109	6	ABO02860 Human sec
21	595	100.0	109	6	ABR75014 Human sec
22	595	100.0	109	6	ABR94776 Human sec
23	595	100.0	109	6	ABU85749 Human PRO
24	595	100.0	109	6	ABU98909 Novel hum
25	595	100.0	109	6	ABU98124 Novel hum

Result ID	Score	Query Match	Length	DB ID	Description
26	595	100.0	109	6	ABU91830 Novel hum
27	595	100.0	109	6	ABU89523 Human PRO
28	595	100.0	109	6	ABU86364 Human PRO
29	595	100.0	109	6	ABU67577 Human sec
30	595	100.0	109	6	ABU80605 Human PRO
31	595	100.0	109	6	ABU90932 Novel hum
32	595	100.0	109	6	ABO33991 Human sec
33	595	100.0	109	6	ABR99523 Human sec
34	595	100.0	109	6	ABR98913 Human sec
35	595	100.0	109	6	ABO16436 Human sec
36	595	100.0	109	6	ABR92336 Human sec
37	595	100.0	109	6	ABO18977 Human sec
38	595	100.0	109	6	ABR78398 Human sec
39	595	100.0	109	6	ABU72008 Novel hum
40	595	100.0	109	6	ABU85134 Novel hum
41	595	100.0	109	6	ABO00273 Novel hum
42	595	100.0	109	6	ABO11605 Human sec
43	595	100.0	109	6	ABO02250 Human sec
44	595	100.0	109	6	ABU88824 Novel hum
45	595	100.0	109	6	ABU83519 Human sec

ALIGNMENTS

Result ID	Score	Query Match	Length	DB ID	Description
RESULT 1					
AAV94964					
AAV94964					standard; protein; 109 AA.
AAV94964					
AAV94964					
16-JUN-2000					(first entry)
Human					secreted protein clone GY442.2 protein sequence SEQ ID NO:134.
Human					secreted protein; immunostimulant; immunosuppressant; virucide;
Human					antifungal; cytosstatic; antiinflammatory; dermatological;
antidiabetic					; antihistaminic; antiarthritic; antirheumatic; protozoacide;
infection					; immune deficiency; severe combined immunodeficiency; SCID;
infection					; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
connective tissue					disease; multiple sclerosis; erythematosis;
rheumatoid arthritis					; autoimmune pulmonary inflammation; asthma;
Gullain-Barre					syndrome; autoimmune thyroiditis; myasthenia gravis;
insulin dependent					diabetes mellitus; graft-versus-host-disease;
autoimmune					inflammatory eye disease; allergy.
Homo sapiens					
WO200009552-A1					
24-FEB-2000					
13-AUG-1999					99WC-US018298.
14-AUG-1998					98US-0096622P.
17-AUG-1998					98US-0096615P.
04-SEP-1998					98US-0099229P.
23-OCT-1998					98US-0105368P.
08-JAN-1999					99US-0115234P.
12-FEB-1999					99US-0119931P.
18-FEB-1999					99US-0120575P.
30-APR-1999					99US-0132020P.
11-AUG-1999					99US-0148424P.
(GEMV) GENETICS INST INC.					
Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;					
Wong GG, Clark HF, Reindel K;					
WPI; 2000-205979/18.					
New polynucleotides encoding secreted proteins, which may have e.g.					

PT nutritional, chemokine, immune stimulating or suppressing, hematopoiesis
 PT regulating, tissue growth, activin/inhibin anti-inflammatory or tumor
 PT inhibition activity.
 PS Claim 143; Page 595; 641pp; English.
 CC AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898
 CC to AAY94980, isolated from human adult brain, adult thyroid, adult
 CC retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult
 CC placenta, adult testis, whole embryo, adult cartilage, kidney, foetal
 CC brain, adult thymus, foetal placenta, adult uterus, adult tumour, and
 CC adult bladder, cDNA libraries. The polynucleotides and proteins are
 CC predicted to have biological activities which would make them suitable
 CC for treating, preventing or ameliorating medical conditions in humans and
 CC animals. The polynucleotides can be used as markers for tissues in which
 CC the protein is preferentially expressed, as molecular weight markers on
 CC Southern gels, and as chromosome markers or tags to identify chromosomes
 CC or to map gene positions. The proteins can be used in the treatment of
 CC immune deficiencies and disorders, such as severe combined
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other
 CC infections. These infections include human immunodeficiency virus (HIV),
 CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
 CC candidiasis. The proteins can be used to treat autoimmune disorders such
 CC as connective tissue disease, multiple sclerosis, systemic lupus
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent
 CC diabetes mellitus, myasthenia gravis, graft-versus-host disease and
 CC autoimmune inflammatory eye disease. The proteins can also be used to
 CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent
 CC probes for the human secreted proteins from the present invention.
 CC
 CC Sequence 109 AA:
 SQ
 * Query March 100.0%; Score 595; DB 3; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-55;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 25-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102886P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 XX (INCY-) INCYTE PHARM INC.
 PI Lal P, Tang YF, Gorsone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Merklow IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI; 2000-160673/14.
 DR N-PSDB; AAZ98229.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
 PS Claim 1; Page 240; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antihistaminic activities, and can be
 CC used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, microbial or other infections, congenital or
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, or triple-acting
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSP are also used to raise
 CC specific antibodies (Ab) and to screen for agonists and antagonists
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
 CC complementary drug screens, and for purification of HSP from natural
 CC sources
 CC
 CC Sequence 109 AA:
 SQ
 * Query March 100.0%; Score 595; DB 3; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-55;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 25-JUN-1998; 98US-0090762P.
 PR 31-JUL-1998; 98US-0094983P.
 PR 01-OCT-1998; 98US-0102886P.
 PR 11-DEC-1998; 98US-0112129P.
 XX
 XX (INCY-) INCYTE PHARM INC.
 PI Lal P, Tang YF, Gorsone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Merklow IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 DR WPI; 2000-160673/14.
 DR N-PSDB; AAZ98229.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
 PS Claim 1; Page 240; 327pp; English.
 XX
 CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antihistaminic activities, and can be
 CC used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, microbial or other infections, congenital or
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, or triple-acting
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSP are also used to raise
 CC specific antibodies (Ab) and to screen for agonists and antagonists
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
 CC complementary drug screens, and for purification of HSP from natural
 CC sources
 CC
 CC Sequence 109 AA:
 SQ

XX Homo sapiens.
OS MO200012708-A2.
XX
XX 09-MAR-2000.
XX
PF 01-SEP-1999; 99WC-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099236P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099744P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100663P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101814P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101478P.
PR 23-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102307P.
PR 29-SEP-1998; 98US-0102310P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.

PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0106500P.
PR 30-OCT-1998; 98US-0106644P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108825P.
PR 17-NOV-1998; 98US-0108825P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.

XX (GETH) GENENTECH INC.
PA Baker K, Goddard A, Gurney AL, Smith V, Matanabe CK, Wood WT;
XX
PI WPI; 2000-237871/20.
XX
DR N-PSDB; AAA37106.
DR
XX
PT New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT PRO polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS Claim 12; Fig 170; 773pp; English.
XX
CC AAA37022 to AAA37144 encode the new isolated human transmembrane,

CC receptor or secreted PRO polypeptides given in AAY9340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC antigenic peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding them have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 595; DB 3; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-55;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMWLVLLIIPTLTKSVFCSTVLSYLPNTEDLSLMLMPKPDHSGTRTEVSTHTVPSKPG 60
 1 MLMWLVLLIIPTLTKSVFCSTVLSYLPNTEDLSLMLMPKPDHSGTRTEVSTHTVPSKPG 60
 Db 1 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109

QY 61 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109
 61 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109
 Db 61 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109

RESULT 4
 AAB6173
 ID AAB6173 standard; protein; 109 AA.
 XX
 AC AAB6173;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Protein of the invention #85.
 DE
 KW Secreted; transmembrane; gene therapy.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004342.
 XX
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Thomas D, Watanabe CK,
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2001-071395/08.
 XX
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX
 PS Claim 1; Fig 170; 787pp; English.
 XX
 CC The present invention relates to secreted and transmembrane proteins,
 CC these proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-

CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 595; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-55;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLMWLVLLIIPTLTKSVFCSTVLSYLPNTEDLSLMLMPKPDHSGTRTEVSTHTVPSKPG 60
 1 MLMWLVLLIIPTLTKSVFCSTVLSYLPNTEDLSLMLMPKPDHSGTRTEVSTHTVPSKPG 60
 Db 1 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109

QY 61 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109
 61 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109
 Db 61 TASPCCWPLAGAVPSPPTVSRLEALTRAVQVAEPVIGSGCGPGGRRRD 109

RESULT 5
 AAU29195
 ID AAU29195 standard; protein; 109 AA.
 XX
 AC AAU29195;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #172.
 DE
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006520.
 XX
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 06-MAR-2000; 2000US-0186568P.
 PR 14-MAR-2000; 2000US-0189320P.
 PR 14-MAR-2000; 2000US-0189328P.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-019114P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194447P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196487P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196620P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000OWO-US014941.
 PR 02-JUN-2000; 2000OWO-US015264.
 PR 05-JUN-2000; 2000OUS-0209832P.
 PR 28-JUL-2000; 2000OWO-US020710.
 PR 22-AUG-2000; 2000OUS-00644848.
 PR 24-AUG-2000; 2000OWO-US023328.
 PR 08-NOV-2000; 2000OWO-US030952.
 PR 01-DEC-2000; 2000OWO-US032678.
 PR 20-DEC-2000; 2000OWO-US034956.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR MPI; 2001-602746/58.
 DR N-PSDB; AAS46096.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 344; 774pp; English.
 XX
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumor in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumor in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumor necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumors and also
 CC susceptibility to tumor development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumors, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 CC
 CC
 SQ Sequence 109 AA;

Query Match 100.0%; Score 595; DB 4; Length 109;
 .. Best Local Similarity 100.0%; Pred. No. 2e-55; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 0;

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 Db 1 MLMWLVLLPPTLKSVFCSLVTSLYLPNTEDLSLWMLMPKRDLSGTRTEVSTHTVPSKPG 60
 QY 61 TASPCCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGCPGRRRD 109
 Db 61 TASPCCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGCPGRRRD 109

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 ID AAB87582 standard; protein; 109 AA.
 AC AAB87582;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1446.
 XX
 DE Human; PRO protein; mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200116318-A2.
 XX
 PD 08-MAR-2001.

24-AUG-2000; 2000OWO-US023328.
 XX
 PF 01-SEP-1999; 99WO-US020111.
 XX
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000OUS-0175481P.
 PR 18-FEB-2000; 2000OWO-US004341.
 PR 18-FEB-2000; 2000OWO-US004342.
 PR 22-FEB-2000; 2000OWO-US004414.
 PR 01-MAR-2000; 2000OWO-US005601.
 PR 03-MAR-2000; 2000OUS-0187202P.
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 PR 25-APR-2000; 2000OUS-0199397P.
 PR 22-MAY-2000; 2000OWO-US014042.
 PR 05-JUN-2000; 2000OUS-0209832P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CU, Gurney AL, Watanabe CK, Wood WI,
 XX
 DR MPI; 2001-183260/18.
 DR N-PSDB; AAF92114.
 XX
 PT Bigly four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX
 PS Claim 12; Fig 114; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridization probes, and in chromosome and gene mapping
 CC
 CC
 SQ Sequence 109 AA;

Query Match 100.0%; Score 595; DB 4; Length 109;
 .. Best Local Similarity 100.0%; Pred. No. 2e-55; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 0;

QY 1 MLMWLVLLPPTLKSVFCSLVTSLYLPNTEDLSLWMLMPKRDLSGTRTEVSTHTVPSKPG 60
 Db 1 MLMWLVLLPPTLKSVFCSLVTSLYLPNTEDLSLWMLMPKRDLSGTRTEVSTHTVPSKPG 60
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 Db 61 TASPCCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGCPGRRRD 109

RESULT 7
 ABG95907
 ID ABG95907 standard; protein; 109 AA.
 AC ABG95907;
 XX
 DT 10-DEC-2002 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1446.
 XX
 DE Human; secreted protein; transmembrane protein; antiinflammatory;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX

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PN   US2002119130-A1.
XX
XX   29-AUG-2002.
XX
XX   06-DEC-2001; 2001US-00006867.
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XX   29-OCT-1997; 97US-0063435P.
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XX   06-OCT-1998; 98US-0103449P.
XX   08-MAR-1999; 99US-05005028.
XX   14-MAY-1999; 99US-05010733.
XX   02-JUN-1999; 99US-05012252.
XX   01-SEP-1999; 99US-05020111.
XX   15-SEP-1999; 99US-05021090.
XX   15-SEP-1999; 99US-05021194.
XX   22-DEC-1999; 99US-05030720.
XX   18-FEB-2000; 2000US-05004341.
XX   18-FEB-2000; 2000US-05004342.
XX   22-FEB-2000; 2000US-05004414.
XX   01-MAR-2000; 2000US-05005601.
XX   30-MAR-2000; 2000US-05008439.
XX   22-MAY-2000; 2000US-05014042.
XX   02-JUN-2000; 2000US-05015264.
XX   23-AUG-2000; 2000US-05023522.
XX   24-AUG-2000; 2000US-05023528.

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PR   10-NOV-2000; 2000US-05030873.
PR   01-DEC-2000; 2000US-05032378.
PR   20-DEC-2000; 2000US-05034956.
PR   28-FEB-2001; 2001US-05006520.
PR   01-MAR-2001; 2001US-05006666.
PR   30-MAY-2001; 2001US-05017443.
PR   01-JUN-2001; 2001US-05017800.
PR   20-JUN-2001; 2001US-05019692.
PR   29-JUN-2001; 2001US-05021066.
PR   09-JUL-2001; 2001US-05021735.
PR
PR   (SETH ) GENENTECH INC.
XX
XX   Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI   Glimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX   WPI; 2002-721348/79.
DR
DR   N-PSDB; ABS74434.
XX
XX   New isolated secreted and transmembrane PRO polypeptide useful for
PT   modulating biological activity of a cell, or for treating sports-related
PT   joint problems, osteoarthritis or rheumatoid arthritis.
XX
XX   Claim 20; Fig 114; 399pp; English.
XX
XX   The invention relates to an isolated secreted and transmembrane PRO
CC   polypeptide having 80 % sequence identity to a sequence appearing as
CC   ABG55651-ABG59534 or their associated signal peptide, or a sequence of an
CC   extracellular domain of the proteins with their associated signal peptide
CC   or lacking its associated signal peptide. Also included are the nucleic
CC   acids encoding the proteins, vectors, host cells, fusion proteins and
CC   antibodies which specifically bind to the proteins. The proteins are
CC   useful for detecting a polypeptide designated as A, B, C or D in a sample
CC   suspected of containing an A, B, C or D polypeptide, by contacting the
CC   sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC   and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC   conjugate in the sample, where the formation of the conjugate is
CC   indicative of the presence of an A, B, C or D polypeptide in the sample,
CC   where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC   PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC   polypeptide, F is a PRO1 polypeptide, G is a PRO30040 polypeptide, H is a
CC   PRO20233 polypeptide and I is a PRO1899 polypeptide. The sample comprises
CC   a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC   H or I polypeptide is labeled with a detectable label or is attached to a
CC   solid support. The proteins are useful for linking a bioactive molecule
CC   to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC   H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC   The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC   or I, or antibodies against them are useful for modulating a biological
CC   activity of a cell expressing a polypeptide designated as A, B, C or D or
CC   E, F, G, H, or I. The cell is killed. The proteins are useful for
CC   identifying agonists or antagonists, for the preparation of a medicament
CC   useful in the treatment of a condition which is responsive to the
CC   proteins, as molecular weight markers for protein electrophoresis
CC   purposes, and as therapeutic agents for treating sports-related joint
CC   problems, articular cartilage defects, osteoarthritis or rheumatoid
CC   arthritis. Nucleic acids encoding the proteins are useful as
CC   hybridisation probes, in chromosome and gene mapping, in the generation
CC   of anti-sense RNA and DNA, for the preparation of the proteins, to
CC   generate transgenic or knockout animals which are useful in the
CC   development and screening of therapeutic useful reagents, for chromosome
CC   identification, and in gene therapy. The antibody is useful as a
CC   therapeutic agent, in a diagnostic assay and for affinity purification of
CC   the protein from recombinant cell culture natural sources. The present
CC   sequence represents a novel secreted or transmembrane protein of the
CC   invention
CC
XX   Sequence 109 AA;
XX
Query Match          100.0%;  Score 595;  DB 5;  Length 109;
Best Local Similarity 100.0%;  Pred. No. 26-55;
Matches 109;  Conservative 0;  Mismatches 0;  Gaps 0;

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Oy 1 MIMWLVLLIPLTKSVFCSLVTSLYLPTNTEDLSIMMIPKPKDLSGRTREVSTHTVPSKFG 60
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RESULT 8

ABU58571 standard; protein; 109 AA.

ABU58571;

ABU58571; (first entry)

15-APR-2003 (first entry)

Human PRO polypeptide #172.

Human: PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
 dog; cat; cow; horse; sheep; pig; goat; rabbit; ADERT;
 antibody-dependent enzyme mediated prodruug therapy.

Homo sapiens.

US2003027272-A1.

06-FEB-2003.

21-JUN-2002; 2002US-00176492.

18-SEP-1997; 97US-0059263P.
 18-SEP-1997; 97US-0059266P.
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PR 02-JUL-1998; 98US-00916262P.
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PR 01-OCT-1998; 98US-01026842P.
PR 01-OCT-1998; 98US-01026872P.
PR 02-OCT-1998; 98US-01029652P.
PR 06-OCT-1998; 98US-01032582P.
PR 06-OCT-1998; 98US-01034492P.
PR 07-OCT-1998; 98US-00168978.

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Query Match 100.0%; Score 595; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 M L M W M V L I L L P T L K S V F C S L V T S I X L P W T E D L S I M L M W K P D L H S G T R T E V S T H T V P S K P G 60

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Qy 61 T A S P C W P L A G A V P S P T V S R I E A L T R A V O V A E P L G S C G F O G G P C P G R R D 109
Db 61 T A S P C W P L A G A V P S P T V S R I E A L T R A V O V A E P L G S C G F O G G P C P G R R D 109

RESULT 9
ABU88119
ABU88119 standard; protein; 109 AA.
XX
AC ABU88119;
XX
DT 07-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein Prol1446.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
OS Homo sapiens.
XX
PN US2003032127-A1.
XX
PD 13-FEB-2003.
XX
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 KW chondrocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiarthritic; vulnery; gene therapy.
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 Db 61 TASPQWPLAGAVSPFVTSRIEALTRAVOVAEPIGSCGPGGPPGRRRD 109

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 KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 KW Chromocyte; proliferation; differentiation; cartilage disorder;
 KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
 KW liver; drug screening; transgenic animal; genetic analysis;
 KW antiherbic; vulnereary; gene therapy.
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 OS Homo sapiens.
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 PD 20-FEB-2003.
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DT 09-AUG-2003 (First entry)
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 KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.
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 OS Homo sapiens.
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Query Match 100.0%; Score 595; DB 6; Length 109;
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 D b 1 M L M M V L L L L P T L K S V F G S L V T S L Y I P N T E D I S L M I M P P E D I H S G R T V S T H T V S K R G 60

QY 61 T A S P C M P L A G A V P S P T V S R L E A L T R A V O V A E P L I G S G F G G P C P G R R D 109
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RESULT 14
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 XX ABU82877;
 AC
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 DT 27-JUN-2003 (first entry)
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 DE Human PRO polypeptide #172.

XX Human; PRO polypeptide; secreted and transmembrane protein; tumour;
 KW Chromosome mapping; gene mapping; cytostatic.
 XX Homo sapiens.
 OS US2003032113-A1.
 XX 13-FEB-2003.
 PD 20-JUN-2002; 2002US-00176911.
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Query Match 100.0%; Score 595; DB 6; Length 109;
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 Db 61 TASPCHPLAGAVPSPTYSRLEALTRAVOVAEPIGSCGCGPQGGRRRD 109

RESULT 15
 ABU89998 standard; protein; 109 AA.
 ID ABU89998;
 AC ABU89998;
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 DT 11-AUG-2003 (first entry)
 XX Novel human secreted and transmembrane protein PRO1446.
 XX Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
 KW Chondrocyte differentiation; tumour necrosis factor-alpha release;
 PR

KW affinity purification.
 XX Homo; sapiens.
 OS US2003036147-A1.
 XX
 PN 20-FEB-2003.
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 PD
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 XX 02-JUL-2002; 2002US-00187741.
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 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102644P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 595; DB 6; Length 109;
 Best Local Similarity 100.0%; Pred. No. 2e-55; 0; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 0;
 Qy 1 M M M V I L I L P T K S V F C S I V T S L V Y P N T E D I S L M I M P K R D L H S G R T E V S T H T V P S K P G 60
 Db 1 M M M V I L I L P T K S V F C S I V T S L V Y P N T E D I S L M I M P K R D L H S G R T E V S T H T V S K P G 60
 Qy 61 T A S P C W P L A G A V P S P T V S R I E A L T R A V O V A E P I G S C G P O G G P C P G R R D 109
 Db 61 T A S P C W P L A G A V P S P T V S R I E A L T R A V O V A E P I G S C G P O G G P C P G R R D 109

Search completed: December 25, 2004, 16:31:07
 Job time : 75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 14:35:27 ; Search time 22 Seconds
(without alignments) 476.710 Million cell updates/sec

Title: US-10-063-728-114

Perfect score: 595
Sequence: 1 MWMWLVLLIPLTKKVFQSL.....AEPDQSCGFGGPGRRRD 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Labeling first 45 summaries

Database : PIR 79:*
1: Pirt1:*
2: Pirt2:*
3: Pirt3:*
4: Pirt4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	14.1	314	2 G95403	probable ABC trans
2	80.5	13.5	217	2 S01358	sallyvary glue prot
3	79.5	13.4	1102	2 JH0717	guanylate cyclase
4	75.5	12.7	393	1 S06594	cellular tumor ant
5	74.5	12.5	555	2 T04146	glyoxyl homolog -
6	73.5	12.4	627	2 D75393	serine proteinase,
7	73	12.3	224	2 C48552	transfer protein b
8	73	12.3	841	2 AG2250	nitrogen assimilat
9	72	12.1	391	2 JC6193	tumor suppressor p
10	71.5	12.0	335	2 T44498	hypothetical prote
11	71.5	12.0	340	1 WMBE11	latency-related pr
12	71.5	12.0	450	2 B82957	probable aminotran
13	71	11.9	845	2 T12537	hypothetical prote
14	70.5	11.8	274	2 T20435	hypothetical prote
15	70.5	11.8	464	2 S75831	hypothetical prote
16	70.5	11.8	553	2 A49364	59 protein, brain
17	70	11.8	440	2 S52895	TYA protein, yeast
18	70	11.8	501	2 C49930	hypothetical prote
19	70	11.8	835	2 S75842	nitrogen assimilat
20	69.5	11.7	503	2 H70509	hypothetical prote
21	69.5	11.7	2055	2 T00093	hypothetical prote
22	69	11.6	120	2 F72643	hypothetical prote
23	69	11.6	259	2 S76205	hypothetical prote
24	69	11.6	522	2 S52216	viral proteinase -
25	68.5	11.5	359	2 B56731	chromatin assembly
26	68.5	11.5	4859	2 S74173	ryanodine receptor
27	68	11.4	1751	2 A45604	major blood-stage
28	67.5	11.3	236	2 F64964	yeap protein - Esc
29	67.5	11.3	453	1 S49013	transforming prote

30	67.5	11.3	615	2 T34392	hypothetical prote
31	67.5	11.3	862	1 UYPVNA	noncapsid protein
32	67.5	11.3	672	2 S33015	hypothetical prote
33	67.5	11.3	992	2 A31666	hypothetical prote
34	67.5	11.3	1215	2 S50428	probable Ca2+-tran
35	67	11.3	130	2 G72609	hypothetical prote
36	67	11.3	441	2 A43555	GAP-43-related pro
37	67	11.3	475	2 G83028	N-acetylmutramoyl-L
38	67	11.3	2629	2 T30987	telomerase-associated
39	66.5	11.2	118	2 S54309	hypothetical 13.2K
40	66.5	11.2	684	2 A53019	collagen alpha 1(X
41	66.5	11.2	982	2 T19171	hypothetical prote
42	66.5	11.2	3566	1 A40701	tenascin-X precurs
43	66	11.1	187	2 T50610	hypothetical prote
44	66	11.1	254	2 S75187	hypothetical prote
45	66	11.1	302	2 T40490	probable 26s prote

ALIGNMENTS

RESULT 1
G95403
probable ABC transporter, ATP-binding protein Sma2079 [imported] - Sinorhizobium meliloti
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: G95403
R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A/Reference number: A95262; MUID:21396509; PMID:11481432
A/Accession: G95403
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-314 <KUR>
A/Cross-references: UNIPROT:Q92XV5; GB:AE006469; PDB:AAK65793.1; PID:g14524294; GSPDB:G
R;Experimental source: strain 1021, megaplasmid pSymA
R/Galber, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federpiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
S/Date: 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kless, E.; Komp, C.; Lelaure,
heault, P.; Vandendri, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Content: annotation
C/Genetics:
A/Genes: Sma2079
A/Genome: plasmid
C/superfamily: inner membrane protein malk; ATP-binding cassette homology

Query Match 14.1%; Score 84; DB 2; Length 314;
Best Local Similarity 30.7%; Pred. No. 0.95;
Matches 27; Conservative 14; Mismatches 29; Indels 18; Gaps 4;

QY 17 FCSLVTSLYL---PMTEDLSIMLWPKPDIHGSTRTEVSTHIVVPSKPGTASCMPLAGAV 72
DB 213 FQDRVIVMYLGRVSVASDDETMSDPR--HPTRALMAAVDPSPRPGAA---PLGGL 266
QY 73 PSPT-----VSRLEALTRAVOVAEP 92
DB 267 PPSNSIPGCRPHTRCPPLATELCRAVAP 294

RESULT 2
S01358
sallyvary glue protein sgs-3 precursor - fruit fly (Drosophila simulans)
C/Species: Drosophila simulans
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C/Accession: S01358; A29388
R/Martin, C.H.; Mayeda, C.A.; Meyerowitz, E.M.
J. Mol. Biol. 201, 273-287, 1988

A>Title: Evolution and expression of the Sgs-3 gene of *Drosophila*.
 A/Reference number: S01358; MUID:98332966; PMID:3138416
 A/Accession: S01358
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-217 <MAR>
 A/Cross-references: UNIPROT:P13729
 C/Genetics:
 A/Gene: Sgs-3
 A/Cross-references: FlyBase:FBgn0012853
 C/Superfamily: salivary glue protein
 F:1-217/Domains: salivary glue protein
 F:24-217/Product: salivary glue protein sgs-3 #status predicted <MAY>

Query Match 13.5%; Score 80.5; DB 2; Length 217;
 Best Local Similarity 29.1%; Pred. No. 1.4;
 Matches 30; Conservative 10; Mismatches 46; Indels 17; Gaps 5;
 QY 11 PTLKSVFCSLVTSYLVNT--EDLSLWLPKPKDLHSGTRTEVSTHTVP-SKP--GTAASP 64
 Db 90 PTKSTSTSTTTTTPAPPTTCKTSTTTTTHKPTTHSTPTKTKPTKPTKPTKPTKPTKPTK 149
 QY 65 CWPLAGAVPSPVSRRLALTRAVQVAREPLG--SCGFGCGGCGPG 105
 Db 150 TKPTKHTTPTTTT-----TPKPCGCKSCGCGGCPCKG 183

RESULT 3

JH0717
 guanylate cyclase (EC 4.6.1.2) 2D precursor, retinal - human
 N/Alternate names: guanylyl cyclase; retinal guanylate cyclase 1
 C/Species: Homo sapiens (man)
 C/Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 09-Jul-2004
 C/Accession: JH0717; A55186
 R:Shivan, A.W.; de Sauvage, F.J.; Gillett, N.A.; Goeddel, D.V.; Lowe, D.G.
 A>Title: Molecular cloning of a retina-specific membrane guanylyl cyclase.
 A/Reference number: JH0717; MUID:93001163; PMID:1356371
 A/Accession: JH0717
 A/Molecule type: mRNA
 A/Residues: 1-1102 <SHY>
 A/Cross-references: UNIPROT:Q02846; GB:M92432
 A/Experimental source: retina
 R:Oliveira, L.; Minou, P.; Viegas-Pequignot, E.; Rozet, J.M.; Dollfus, H.; Pittler, S.J.
 Genomics 22, 478-481, 1994
 A>Title: Human retinal guanylate cyclase (GUC2D) maps to chromosome 17p13.1.
 A/Reference number: A55186; MUID:95104866; PMID:7806240
 A/Accession: A55186
 A/Molecule type: DNA
 A/Residues: 1001-1087 <OLI>
 A/Cross-references: GB:L26921
 C/Genetics:
 A/Gene: GDB:GUC2D
 A/Cross-references: GDB:136012; OMIM:600179
 A/Map position: 17p13-17p13
 C/Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homolog
 C/Keywords: GMP biosynthesis; glycoprotein; phosphorus-oxygen lyase; transmembrane protein
 F:1-51/Domains: signal sequence #status predicted <SIG>
 F:53-1102/Product: guanylate cyclase #status predicted <MAY>
 F:463-487/Domains: transmembrane #status predicted <TMM>
 F:524-811/Domains: protein kinase homolog <KIN>
 F:851-1059/Domains: guanylate cyclase catalytic domain homology <GCC>

Query Match 13.4%; Score 79.5; DB 2; Length 1102;
 Best Local Similarity 24.8%; Pred. No. 10;
 Matches 39; Conservative 13; Mismatches 46; Indels 59; Gaps 7;

QY 3 WW-----LVLLLL-PTLKSVF-----CSLVTSYLVLPNTEDLSR 34
 Db 21 WMAPSLPRLPRLPRLPLRLLDLPALSAVFTVGVLPWACDPIFSARP---DLAA 77
 QY 35 WLP-----KPDHSGTRTEVSTHTVPSK-----GTAACWPLAGA 71

Db 78 RLAAARINRDPGLAGGPRREVALLPKCRTPGSLGAVSSALARVSGLVGVPVNC-----G 132
 QY 72 VPSPTVSRLEALTRAVQVAREPLGSCGFGCGGCPGRRR 108
 Db 133 LPASRAARRSRPRLAGALGLPDDAGGHHGPRCPDR 169

RESULT 4

S06594
 cellular tumor antigen p53 - green monkey
 C/Species: Cercopithecus aethiops (green monkey, griwet)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: S06594
 R:Rigaudi, P.; Eckhart, W.
 Nucleic Acids Res. 17, 8375, 1989
 A>Title: Nucleotide sequence of a cDNA encoding the monkey cellular phosphoprotein p53.
 A/Reference number: S06594; MUID:90045967; PMID:2530498
 A/Accession: S06594
 A/Molecule type: mRNA
 A/Residues: 1-393 <SIG>
 A/Cross-references: UNIPROT:P13481; EMBL:X16384; NID:G22795; PID:CAA34420.1; PID:G22796
 C/Superfamily: cellular tumor antigen p53
 C/Keywords: apoptosis; cell division control; DNA binding; homeotetramer; nucleus; phospho
 F:176,179,238,242/Binding site: zinc (Cys, His, Cys) #status predicted
 F:392/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match

12.7%; Score 75.5; DB 1; Length 393;
 Best Local Similarity 30.1%; Pred. No. 8.1;
 Matches 34; Conservative 12; Mismatches 32; Indels 35; Gaps 8;
 QY 2 LWWL-----VLLLLPTLKSVCSTLVSTLVLPNTEDLSLW--PKEDLHSGTRTEVSTH- 53
 Db 22 LWWLLENNVTLPLPS-----QAVDLDLW-SPDILAQVLTEDDPPD--EAPRWSEAAPM 73
 QY 54 -TVPSKPTGASPC---WPLAGAVPSPVSRRLALTRAVQVAREPLGSCGFGCGG 101
 Db 74 APTPAAPTPAAPAPAPSWPLSSVPSQKTYR-----GSYGFRLG 112

RESULT 5

T04146
 gliosyl homolog - rice (Fragment)
 C/Species: Oryza sativa (rice)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T04146
 R:Hansen, J.D.; Pye, J.; Xia, Y.; Men, T.J.; Robertson, D.S.; Kolatukudy, P.E.; Nikolai
 Plant Physiol. 113, 1091-1100, 1997
 A>Title: The gliosyl locus of maize and an epidermis-specific cDNA from *Kleinsinia odorata*
 A/Reference number: Z14699; MUID:97267140; PMID:9112770
 A/Accession: T04146
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-555 <HAN>
 A/Cross-references: UNIPROT:O04693; EMBL:U57338; NID:G2213642; PID:NAA87722.1; PID:G2212
 C/Experimental source: cv. Nipponbare
 C/Superfamily: Arabidopsis thaliana hypothetical protein F13M22.20

Query Match 12.5%; Score 74.5; DB 2; Length 555;
 Best Local Similarity 30.9%; Pred. No. 15;
 Matches 30; Conservative 10; Mismatches 44; Indels 13; Gaps 6;

QY 3 W-VLWLLLLPTLKSVCSTLVSTLVLPNTEDLSLWLPKPKDLHSGTRTEVSTHTVPSKPGT 61
 Db 25 WMDMMVMVMQTL--IAAVLVTSRVPAPASDLSAM-----DLR-GWAIIVLVHVAVSEPAF 76
 QY 62 ASPCWPLAGAVPSPVSRRLALTRAVQVAREPLGSCGFG 98
 Db 77 ---YWAHRAIHGIPLSFRVYSHHSFOATQAL-TAGF 109
 RESULT 6
 D75393
 serine proteinase, subtilase family - *Deinococcus radiodurans* (strain R1)

Qy 9 LLPTLKSVEFGSLVTSYLPTEDLSLMLMKPDLHSGTRTEVSTHTVPSKRGTAASPCWPL 68
 Db 88 LARLADAFWPGPRTLLLPSSAQV-----PDADVTSGRATVGLR-VPDQVALALIERP 139
 Qy 69 AGAVSPPTVSRLEAL--TRAVQVAEPLG---SCGFQGGPC 103
 Db 140 GGGIAAAPSANRFGVSPPTTAHVAAADLGDVVDLVLDGGPC 179

RESULT 11

MBR11
 latency-related protein 1 - human herpesvirus 1 (strain F)
 C:Species: human herpesvirus 1
 A:Note: host Homo sapiens (man)
 C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 C/Accession: A33337
 R:Wechsler, S.L.; Neuhorn, A.B.; Zwaagstra, J.; Ghiasi, H.
 Virology 168, 168-172, 1989
 A:Title: Sequence of the latency-related gene of herpes simplex virus type 1.
 A:Reference number: A94388; MUID:89085598; PMID:2553901
 A/Accession: A33337
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-340 <MRC>
 A:Cross-references: UNIPROT:P17588; GB:J04323; NID:G330133; PIDN:AAA45799.1; PID:G330134
 C:Genetics: 249/2
 A:Introns:
 C:Superfamily: herpesvirus latency-related protein 1
 C:Keywords: tandem repeat
 F:26-41/Region: 16-residue tandem repeat
 F:42-57/Region: 16-residue tandem repeat
 E:58-73/Region: 16-residue tandem repeat

Query Match 12.0%; Score 71.5; DB 1; Length 340;
 Best Local Similarity 37.1%; Pred. No. 17;
 Matches 23; Conservative 5; Mismatches 29; Indels 5; Gaps 3;

Qy 33 SLMLMPKRDLSGTRTEVSTHTVPSKRGTAASPCWPLAGAVSPPTVSRLEALTRAVQVAE 91
 Db 14 ALMLTPEPAQH-GTPPTPHSHAPPLDRPTPSHSHRAPLDP--RAPPTPHSHAP 69
 Qy 92 PL 93
 Db 70 PL 71

RESULT 12
 B82957
 Probable aminotransferase PA5523 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C/Accession: B82957
 R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.T.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A/Accession: B82957
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450 <STO>
 A:Cross-references: UNIPROT:Q9HT50; GB:AE004964; GB:AE004091; NID:G9951849; PIDN:AA08990
 A:Experimental source: strain PA01
 C:Genetics: PA5523

Query Match 12.0%; Score 71.5; DB 2; Length 450;
 Best Local Similarity 26.6%; Pred. No. 23;
 Matches 21; Conservative 9; Mismatches 28; Indels 21; Gaps 3;

Qy 38 PKPDLHS-----GRTTEV-STHTVPSKRGTAASPCW-----PLAGAVSPPT 76

Db 221 PGGFHFQKRLRELRHGGTLLIIDFHTTISTGGGGCPRAWKLEPPDFTLCKPIAGVPCSV 280
 Qy 77 VSRLEALTRAVQVAEPLG 95
 Db 281 YGGSAAAMASAMQIARARAS 299

RESULT 13

T12537
 hypothetical protein DKFZp434H244.1 - human (fragments)
 C:Species: Homo sapiens (man)
 C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
 C/Accession: T12537
 R:Mamburt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z17524
 A/Accession: T12537
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-313:314-845 <MAW>
 A:Cross-references: UNIPROT:O14841; EMBL:AL096750
 A:Experimental source: adult testis; clone DKFZp434H244
 A:Note: the cDNA sequence contains a -1 frameshift near codon 313
 C:Genetics:
 A:Note: DKFZp434H244.1
 C:Superfamily: hypothetical protein YKL215c

Query Match 11.9%; Score 71; DB 2; Length 845;
 Best Local Similarity 33.3%; Pred. No. 51;
 Matches 24; Conservative 6; Mismatches 38; Indels 4; Gaps 2;

Qy 33 SLMLMPKRDLSGTRTEVSTHTVPSKRGTAASPCWPLAGAVSPPTVSRLEALTRAVQVAE 92
 Db 42 SLMLGSSQ--QERTQDPRPATAKVRYVIMPAWCPPLAAGPAPVPSPIAAVSCSPASSP 99
 Qy 93 LG--SCGFQGGP 102
 Db 100 QAPHPVHLPGGP 111

RESULT 14
 T20435
 hypothetical protein E03G2.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T20435
 R:KcMurray, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19275
 A/Accession: T20435
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-274 <MIL>
 A:Cross-references: UNIPROT:Q27276; EMBL:Z68113; PIDN:CAA92149.1; GSPDB:GN00028; CESP:E03G2
 A:Experimental source: clone E03G2
 C:Genetics:
 A:Gene: CESP:E03G2.3
 A:Map position: X
 A:Introns: 42/3; 89/2; 197/3; 239/3

Query Match 11.8%; Score 70.5; DB 2; Length 274;
 Best Local Similarity 26.8%; Pred. No. 17;
 Matches 34; Conservative 17; Mismatches 43; Indels 33; Gaps 6;

Qy 5 LVLLILPTLKSVCGLVTSYL-----PNTEDLSLMLMPKRDLSGTRTEVSTHTVPS 57
 Db 3 LVLLILPTLTSIVCALDTAAVTAIQTEINKHSADIMIL-----DHVKININARVSDIGRPG 58

Qy 58 KPQT-ASPCWP-----LAGAVSPPTVSRLEAL--TRAVQV-AEPLG 95
 Db 59 PFGTNGSPGFGSKGRKGRSDGKCSVAVGLVSLDKKKEVETLEFIDSSRETFPYLRLIAN 118

QY 96 CGFQGGP 102
 DB 119 PGRGQP 125

RESULT 15

S/75831
 Hypothetical protein e1r1285 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S75831
 R:Kaneko, T.; Sato, S.; Katani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

B:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75831
 A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-464 <KAN>

A:Cross-references: UNIPROT:P74199; EMBL:D90913; GB:AB001339; NID:G1653348; PIDN:BA11829

A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:start codon: GTG

Query Match 11.8%; Score 70.5; DB 2; Length 464;
 Best Local Similarity 31.1%; Pred. No. 30;

Matches 28; Conservative 8; Mismatches 45; Indels 9; Gaps 2;

QY 13 LKSVFCSLVTSLYLPNTEDLSL-----MLMPKPDLSGSTRTEVSTHTVPSKPGTASPC 65
 DB 159 LQQAWLSLQARLKYGSLPDLISLQKTIIAFNFPQDFRLVTVYFGQLMLDYQENPNVTLPPC 218
 QY 66 WPLAGAVPSPTVSRLEALTRAVQVAEPLGS 95
 DB 219 QEQESAEPSPDVELLQALTRH--EVRTPLTS 246

Search completed: December 25, 2004, 16:31:36
 Job time : 24 secs

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OM protein - protein search, using sw model

Run on: December 25, 2004, 16:11:02 ; Search time 93 Seconds
(Without alignments)
674.364 Million cell updates/sec

Title: US-10-063-728-114
Perfect score: 595
Sequence: 1 MLMWLVLLPLPTLTKSVFCSL.....APBLGSCGFGGPPRRRD 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	595	100.0	109	2	O6UW64	06UW64 homo sapien
2	595	100.0	109	2	AAQ89316	AAQ89316 homo sapi
3	93	15.6	414	2	Q6VIL8	Q6VIL8 streptomyce
4	93	15.6	414	2	AAQ84166	AAQ84166 streptomy
5	92	15.5	391	1	P53 CANPA	Q29537 canis famil
6	84.5	14.2	285	2	O95326	O95326 canis famil
7	84.5	14.2	386	1	P53 FELCA	P1685 felis silve
8	84	14.1	314	2	O92XV5	O92XV5 thizobium m
9	80.5	13.5	217	1	SGS3_DROSI	P13729 drosophilla
10	80.5	13.5	269	1	HXA9_MORSA	O9PW65 morone saxa
11	79.5	13.4	690	2	O8PE82	O8PE82 xanthomonas
12	77.5	13.0	536	2	O93078	O93078 rhodococcus
13	77	12.9	554	2	O9PBH3	O9PBH3 streptococc
14	76.5	12.9	401	2	O8XSC3	O8XSC3 aspergillus
15	76	12.8	369	2	O8NCD7	O8NCD7 salictonia s
16	75.5	12.7	267	2	O9PVQ7	O9PVQ7 oryzae lac
17	75.5	12.7	393	1	P53_CERAE	P13481 cercopithe
18	75.5	12.7	769	2	O9KK24	O9KK24 streptococc
19	75.5	12.7	769	2	O9KK40	O9KK40 streptococc
20	75.5	12.7	769	2	O9PDD1	O9PDD1 streptococc
21	75.5	12.7	2894	2	O9VPE1	O9VPE1 drosophilla
22	75	12.6	329	2	O8ZNI5	O8ZNI5 salictonia s
23	75	12.6	551	2	O8XWP1	O8XWP1 oryzae saliv
24	74.5	12.5	387	2	O04693	O04693 oryzae saliv
25	74	12.4	387	2	O8SP23	O8SP23 delphinapte
26	74	12.4	493	2	O7MAS1	O7MAS1 bordetella
27	74	12.4	493	2	O7W697	O7W697 bordetella
28	73.5	12.4	644	2	O8BBK2	O8BBK2 mus musculu
29	73.5	12.4	515	2	O6P227	O6P227 xenopus tro
30	73.5	12.4	515	2	AAH64237	Ah64237 xenopus t
31	73.5	12.4	627	2	O9RUD0	O9RUD0 deinococcus

Result ID	Score	Query Match	Length	DB ID	Description	
32	73.5	12.4	565	2	O8SYW7	O8SYW7 drosophilla
33	73.5	12.4	710	2	O8POX0	O8POX0 xanthomonas
34	73.5	12.4	886	2	O9VTK2	O9VTK2 drosophilla
35	73.5	12.4	1213	2	O8LSS4	O8LSS4 oryzae saliv
36	73	12.3	224	2	O07193	O07193 streptomyce
37	73	12.3	841	2	O8YR90	O8YR90 anabaena sp
38	72.5	12.2	431	2	O6Z0G5	O6Z0G5 oryzae saliv
39	72.5	12.2	431	2	BAD03641	BAD03641 oryzae sat
40	72.5	12.2	431	2	BAD12953	BAD12953 oryzae sat
41	72	12.1	391	1	P53_RABIT	O95330 oryctolagus
42	72	12.1	1162	1	O6DFY6	O6DFY6 mus musculu
43	72	12.1	1162	1	FXLB_HUMAN	O9Y2K7 homo sapien
44	72	12.1	1162	2	AAH64360	Ah64360 homo sapi
45	71.5	12.0	217	2	O6SL40	O6SL40 arm1111fer

ALIGNMENTS

Result ID	Score	Query Match	Length	DB ID	Description
RESULT 1					
O6UW64					
AC	O6UW64	PRELIMINARY;	PRT;	109 AA.	
AD	O6UW64				
DT	05-JUL-2004 (T-EMBLrel. 27, Created)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)				
DE	PINK1.				
GN	ORFNames=UNG740;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22887296; PubMed=12975309;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,				
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Matk M., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Seshgiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,				
RA	Vandlen R., Watnabe C., Wleand D., Woods K., Xie M.H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P.,				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment."				
RL	Genome Res. 13:2265-2270(2003).				
DR	EMBL: AY358957; AAQ89316.1; -				
SO	SEQUENCE 109 AA; 11822 MW; A8A6C475792E2B73 CRC64;				
Query Match	100.0%; Score 595; DB 2; Length 109;				
Best Local Similarity	100.0%; Pred. No. 1.9e-47;				
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 MLMWLVLLPLPTLTKSVFCSLVTSLYPTNTEDSLIMMPKPDLSGRTVSTHTVPSKPG 60				
Db	1 MLMWLVLLPLPTLTKSVFCSLVTSLYPTNTEDSLIMMPKPDLSGRTVSTHTVPSKPG 60				
Qy	1 TASPFWPLGAVSPPTVSRLEALTRAVOVAEPLGSCGFGGPPRRRD 109				
Db	61 TASPFWPLGAVSPPTVSRLEALTRAVOVAEPLGSCGFGGPPRRRD 109				
RESULT 2					
AAQ89316	PRELIMINARY;	PRT;	109 AA.		
AAQ89316					
02-MAR-2004 (T-EMBLrel. 27, Created)					
02-MAR-2004 (T-EMBLrel. 27, Last sequence update)					
02-MAR-2004 (T-EMBLrel. 27, Last annotation update)					
PINK1.					
UNG740.					

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12975309;
 RA Clark H.F., Gurrey A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Gimaldi C., Gu Q., Hass P.E., Helgens S.,
 RA Hwang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagte A.,
 RA Vandlan R., Warnabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RA "The secreted Protein Discovery Initiative (SPDI), a Large-Scale
 RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 RT Bioinformatics Assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358957; AA089316.1; -
 SQ SEQUENCE 109 AA; 11822 MW; ABA6C475792E2B73 CRC64;

Query Match 100.0%; Score 595; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.9e-47;
 Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWMVLLVLLPPTLTKSVFCSLVTSIYLPTNEDLSLWMPKPDHSGRTTEVSTHVPKRG 60
 DB 1 MLWVLLVLLPPTLTKSVFCSLVTSIYLPTNEDLSLWMPKPDHSGRTTEVSTHVPKRG 60
 61 TASPCCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGPGCPGR 109
 61 TASPCCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGPGCPGR 109

RESULT 3
 ID Q6V1L8 PRELIMINARY; PRT; 414 AA.

AC Q6V1L8 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DR P1MS4.
 GN Name=P1MS4;
 OS Streptomyces sp. HK803;
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=244967;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HK803;
 RC MEDLINE=22841069; PubMed=12819191;
 RA Palanappan N., Kim B.S., Sekiyama Y., Osada H., Reynolds K.A.;
 RT "Enhancement and selective production of phosloactomycin B, a protein
 RT phosphatase IIA inhibitor, through identification and engineering of
 RT the corresponding biosynthetic gene cluster.";
 RL J. Biol. Chem. 278:35552-35557(2003).
 DR EMBL; AY354515; AA084166.1; -
 DR InterPro; IPR007114; MFS.
 DR PROSITE; PS50850; MFS; 1.
 SQ SEQUENCE 414 AA; 42040 MW; 90604A1085F6C6F5 CRC64;

Query Match 15.6%; Score 93; DB 2; Length 414;
 Best Local Similarity 29.9%; Pred. No. 2.3;
 Matches 35; Conservative 12; Mismatches 42; Indels 28; Gaps 5;

QY 3 WMLVLLVLLPPTLTKSVFCSLVTSIYLPTNEDLSLWMPKPDHSGRTTEVSTH 53
 DB 108 WMPVVVVV-----ALVTGLSAVPSVQISRAVWPKIVGSELSTLYTAATASVIT 159
 54 TVPSKP---GTASPCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGPGCPGR 106

DB 160 TGPLLASLVIAVAGPYWAVG-----VTPALLVLSALVFAAALGKAVGGEPLPQR 209

RESULT 4

ID AA084166 PRELIMINARY; PRT; 414 AA.
 AC AA084166;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE P1MS4.
 GN P1MS4.
 OS Streptomyces sp. HK803;
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=244967;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HK803;
 RC MEDLINE=22841069; PubMed=12819191;
 RA Palanappan N., Kim B.S., Sekiyama Y., Osada H., Reynolds K.A.;
 RT "enhancement and selective production of Phosloactomycin B, a Protein
 RT Phosphatase IIA Inhibitor, through Identification and Engineering of
 RT the Corresponding Biosynthetic Gene Cluster.";
 RL J. Biol. Chem. 278:35552-35557(2003).
 DR EMBL; AY354515; AA084166.1; -
 SQ SEQUENCE 414 AA; 42040 MW; 90604A1085F6C6F5 CRC64;

Query Match 15.6%; Score 93; DB 2; Length 414;
 Best Local Similarity 29.9%; Pred. No. 2.3;
 Matches 35; Conservative 12; Mismatches 42; Indels 28; Gaps 5;

QY 3 WMLVLLVLLPPTLTKSVFCSLVTSIYLPTNEDLSLWMPKPDHSGRTTEVSTH 53
 DB 108 WMPVVVVV-----ALVTGLSAVPSVQISRAVWPKIVGSELSTLYTAATASVIT 159
 54 TVPSKP---GTASPCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGPGCPGR 106
 160 TGPLLASLVIAVAGPYWAVG-----VTPALLVLSALVFAAALGKAVGGEPLPQR 209

RESULT 5

ID P53_CANFA STANDARD; PRT; 381 AA.
 AC Q29337; Q9TV78;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN Name=p53; Synonyms=p53;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canids; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RC MEDLINE=98178696; PubMed=9519881;
 RA Veldhoen N., Milner J.;
 RT "Isolation of canine p53 cDNA and detailed characterization of the
 RT full length canine p53 protein.";
 RL Oncogene 16:1077-1084(1998).
 RN [2]

Query Match 25-300 FROM N.A.
 Best Local Similarity 25-300 FROM N.A.
 Matches 35; Conservative 12; Mismatches 42; Indels 28; Gaps 5;

QY 3 WMLVLLVLLPPTLTKSVFCSLVTSIYLPTNEDLSLWMPKPDHSGRTTEVSTH 53
 DB 108 WMPVVVVV-----ALVTGLSAVPSVQISRAVWPKIVGSELSTLYTAATASVIT 159
 54 TVPSKP---GTASPCWPLAGAVPSPVSRLEALTRAVQVAEPLGSCGFGGPGCPGR 106

RX MEDLINE=95323915; PubMed=7600529;
 RA Kraegel S.A., Pazzi K.A., Madewell B.R.;
 RT Sequence analysis of canine p53 in the region of exons 3-8.;
 RL Cancer Lett. 92:181-186(1995).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and P48 antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- COFACTOR: Binds zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- PTM: Phosphorylated on Thr-18 by VRK1, which may prevent the
 CC interaction with MDM2 (By similarity).
 CC -1- PTM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
 CC induce proapoptotic program and modulate cell senescence (By
 CC similarity).
 CC -1- DISASB: p53 is found in increased amounts in a wide variety of
 CC transformed cells. p53 is frequently mutated or inactivated in
 CC many types of cancer.
 CC -1- SIMILARITY: Belongs to the p53 family.
 CC -----
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 CC -----
 CC EMBL; AF060514; AAC16909.1; -;
 CC EMBL; AB020761; BAA78379.1; -;
 CC EMBL; S77819; AAB42022.1; -;
 CC HSSP; P04637; IGZH.
 CC DR InterPro: IPR002117; P53.
 CC DR InterPro: IPR008967; P53_Like_DNA_bnd.
 CC DR InterPro: IPR010991; P53_tetramerisun.
 CC DR Pfam; PF00870; P53; 1.
 CC DR PRINTS; PR00386; P53SUPPRESSR.
 CC DR PRODOM; PD002681; P53; 1.
 CC DR PROSITE; PS00348; P53; 1.
 CC KW Acetylation; Activator; Anti-oncogene; Apoptosis; DNA-binding;
 CC Metal-binding; Nuclear protein; Phosphorylation;
 CC Transcription regulation; Zinc.
 CC FT DOMAIN 1 44 Transcription activation (acidic).
 CC FT DNA_BIND 89 280 By similarity.
 CC FT DOMAIN 313 344 Oligomerization.
 CC FT DOMAIN 327 338 Nuclear export signal (By similarity).
 CC FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 293 309 Bipartite nuclear localization signal (By
 CC similarity).
 CC FT METAL 163 163 Zinc (By similarity).
 CC FT METAL 166 166 Zinc (By similarity).
 CC FT METAL 226 226 Zinc (By similarity).
 CC FT METAL 230 230 Zinc (By similarity).
 CC FT MOD_RES 15 15 Phosphoserine (by PPPK) (By similarity).
 CC FT MOD_RES 18 18 Phosphothreonine (by VRK1) (By
 CC similarity).
 CC FT MOD_RES 361 361 N6-acetyllysine (By similarity).
 CC FT MOD_RES 370 370 N6-acetyllysine (By similarity).
 CC FT BINDING 380 380 RNA (covalent) (By similarity).
 CC FT CONFLICT 1 4 MERS -> MQEP (in Ref. 2).
 CC FT CONFLICT 378 378 L -> P (in Ref. 2).
 CC FT SEQUENCE 381 AA; 42486 MW; 761A718FDCC3DA59 CRC64;

QY 9 LLP---TLKSFVCLVTLVLPNTEDLSLWMPKRDLSGRTREVSTHTVPSKPGTASRC 65
 Db 25 LIPENNVLSSSELCPAVDLILP--SSVVMWL-----DESDDAPRMPATSAPTAPGPA--PS 77
 QY 66 WPLAAGVPS 75
 Db 78 WPLSSVPS 87
 RESULT 6
 ID Q95326 PRELIMINARY; PRT; 285 AA.
 AC Q95326;
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE P53 protein (Fragment).
 GN Name=P53;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang B.J., Shi X.B., Lau D.H.M.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and P48 antigen expression, or by repression of Bcl-2
 CC expression (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- SIMILARITY: Belongs to the p53 family.
 CC -----
 CC EMBL; U62133; AAB16961.1; -;
 CC HSSP; P04637; IGZH.
 CC DR GO; GO:0005634; C:nucleus; IEA.
 CC DR GO; GO:0003700; F:transcription factor activity; IEA.
 CC DR GO; GO:0006915; P:apoptosis; IEA.
 CC DR GO; GO:0045786; P:negative regulation of cell cycle; IEA.
 CC DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
 CC DR InterPro; IPR002117; P53.
 CC DR InterPro; IPR008967; P53_Like_DNA_bnd.
 CC DR Pfam; PF00870; P53; 1.
 CC DR PRINTS; PR00386; P53SUPPRESSR.
 CC DR PRODOM; PD002681; P53; 1.
 CC DR PROSITE; PS00348; P53; 1.
 CC KW Activator; Anti-oncogene; Apoptosis; Cell cycle; DNA-binding;
 CC Metal-binding; Nuclear protein; Phosphorylation;
 CC Transcription regulation; Zinc.
 CC FT NON_TER 1 1
 CC FT NON_TER 285 285
 CC FT SEQUENCE 285 AA; 31616 MW; 673427DBBFB8BCC6 CRC64;

Query Match 14.2%; Score 84.5; DB 2; Length 285;
 Best Local Similarity 37.7%; Pred. No. 9.4;
 Matches 23; Conservative 6; Mismatches 25; Indels 7; Gaps 3;

P53_FELICA STANDARD; PRT; 386 AA.
 ID P53_FELICA
 AC P41685
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cellular tumor antigen p53 (Tumor suppressor p53).
 GN Name:TP53; Synonyms:TRP53;
 OS Fells silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OC NCI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TTSU=LYmph node;
 RX MEDLINE=94333960; PubMed=8056458;
 RA Okuda M., Umeda A., Sakai T., Ohashi T., Momoi Y., Youn H.Y.,
 RA Watarai T., Goiteuka R., Tsujimoto H., Hasegawa A.;
 RT "Cloning of feline p53 tumor-suppressor gene and its aberration in
 RT hematopoietic tumors.";
 RL Int. J. Cancer 58:602-607(1994).
 RN [2]
 RP SEQUENCE OF 34-354 FROM N.A.
 RX MEDLINE=94114699; PubMed=8286534;
 RA Okuda M., Umeda A., Matsumoto Y., Momoi Y., Watarai T., Goiteuka R.,
 RA O'Brien S.J., Tsujimoto H., Hasegawa A.;
 RT "Molecular cloning and chromosomal mapping of feline p53 tumor
 RT suppressor gene.";
 RL J. Ver. Med. Sci. 55:801-805(1993).
 CC -1- FUNCTION: Acts as a tumor suppressor in many tumor types; induces
 CC growth arrest or apoptosis depending on the physiological
 CC circumstances and cell type. Involved in cell cycle regulation as
 CC a trans-activator that acts to negatively regulate cell division
 CC by controlling a set of genes required for this process. One of
 CC the activated genes is an inhibitor of cyclin-dependent kinases.
 CC Apoptosis induction seems to be mediated either by stimulation of
 CC BAX and P49 antigen expression, or by repression of Bcl-2
 CC expression.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Binds DNA as a homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -1- PFM: Phosphorylated on Thr-18 by VRK1, which may prevent the
 CC interaction with MDM2 (By similarity).
 CC -1- PFM: Acetylated. Its deacetylation by SIRT1 impairs its ability to
 CC induce proapoptotic program and modulate cell senescence (By
 CC similarity).
 CC -1- DISEASE: p53 is found in increased amounts in a wide variety of
 CC transformed cells. p53 is frequently mutated or inactivated in
 CC many types of cancer.
 CC -1- SIMILARITY: Belongs to the p53 family.
 CC -----
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 CC -----
 CC EMBL; D26608; BAA05653.1; -;
 CC EMBL; D16460; BAA03927.1; -;
 CC HSSP; P04637; 1GZH.
 DR InterPro: IPR002117; P53.
 DR InterPro: IPR008967; P53_like_DNA_bnd.
 DR InterPro: IPR010991; P53_Tetramerism.
 DR Pfam; PF00870; P53; 1.
 DR PRINTS; PR00386; P53SUPRBSR.
 DR ProDom; PD002681; P53; 1.
 DR PROSITE; PS00348; P53; 1.
 DR Acetylation; Activator; Anti-oncogene; Apoptosis; DNA-binding;
 KW Metal binding; Nuclear protein; Phosphorylation;
 KW Transcription regulation; Zinc.
 FT DOMAIN 1 44 Transcription activation (acidic).
 FT

FT DNA_BIND 94 285 By similarity.
 FT DOMAIN 318 349 Oligomerization.
 FT DOMAIN 332 343 Nuclear export signal (By similarity).
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 298 314 Bipartite nuclear localization signal (By
 FT similarity).
 FT METAL 168 168 Zinc (By similarity).
 FT METAL 171 171 Zinc (By similarity).
 FT METAL 231 231 Zinc (By similarity).
 FT METAL 235 235 Zinc (By similarity).
 FT MOD_RES 15 15 Phosphoserine (By PEPK) (By similarity).
 FT MOD_RES 18 18 Phosphothreonine (By VRK1) (By
 FT similarity).
 FT MOD_RES 366 366 N6-acetyllysine (By similarity).
 FT MOD_RES 375 375 N6-acetyllysine (By similarity).
 FT BINDING 385 385 RNA (covalent) (By similarity).
 FT CONFLICT 285 285 K -> R (in Ref. 2).
 SQ SEQUENCE 386 AA; 42692 MW; 08B843BA1BC8E878 CRC64;
 Query Match 14.2%; Score 84.5; DB 1; Length 386;
 Best Local Similarity 37.5%; Pred. No. 13;
 Matches 27; Conservative 10; Mismatches 24; Indels 11; Gaps 4;
 Qy 9 LPEPTKSVFCSLVTSLY--LPNTEDLSLWMPKRDHSGTRTEVSHTVPSKPGTASP- 65
 Db 25 LPE--NVVLSSEISSAMNDELPLSEDEVANWDEAPDASG---MSAVPAPAPAPATPAP 79
 Qy 66 ---WPLAGAVPS 74
 Db 80 AISMPLSSFPVS 91
 RESULT 8
 Q92XV5 PRELIMINARY; PRT; 314 AA.
 AC Q92XV5
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Probable ABC transporter, ATP-binding protein.
 GN OrderedListNames=RA1135; ORFNames=SGA2070.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymA.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Gallibert F., Guzy J.,
 RA Garjal M., Hong A., Hutzler L., Hyman R.W., Kahn M.L.,
 RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federapfel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymA megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21368234; PubMed=11474104;
 RA Gallibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
 RA Barloy-Hubler F., Barnett M.J., Becker A., Baistard P., Bothe G.,
 RA Boutry M., Bowser L., Bunimwelter U., Cadieu E., Capela D., Chain P.,
 RA Cowie A., Davis R.W., Dreano S., Federapfel N.A., Fisher R.F.,
 RA Gloux S., Godrie T., Goffeau A., Golding B., Guzy J., Gujral M.,
 RA Hernandez-Lucas I., Hong A., Hutzler L., Hyman R.W., Jones T., Kahn D.,
 RA Kahn M.L., Kaiman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
 RA Masny D., Palm C., Peck M.C., Pohl T.M., Poretzel M., Punelle B.,
 RA Ramsperger U., Surzycki R., Theault P., Vandewol M.,
 RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
 RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";
 RT

RL Science 293:668-672(2001).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AB007299; AKR65793.1; -
 DR PIR; G95403; G95403.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transporter; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR010066; O1:go_HPY_C.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; T.
 DR TIGRFAMs; TIGR01727; O1:go_HPY; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome; Plasmid.
 SQ SEQUENCE 314 AA; 34511 MW; F66596829AD2573 CRC64;

Query Match 14.1%; Score 84; DB 2; Length 314;
 Best Local Similarity 30.7%; Pred. No. 12;
 Matches 27; Conservative 14; Mismatches 29; Indels 18; Gaps 4;

QY 17 FCSLVTSLVY---PMTEDLSLMLWPKPDHSGRTREVSHTVPSKRGTAASPCWPLAGAV 72
 DB 213 FCRRLVLMVILGRVVESSDNTLMSDPR--HPYTRALMAAVPDPSPRQAAA---PLGGEL 266

QY 73 PSPPT-----VSRLEALTRAVQVAEP 92
 DB 267 PPSPSNIPGCRFHTRCPLATELGRVAEP 294

RESULT 9
 SGG3_DROSI STANDARD; PRT; 217 AA.
 AC P13729;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Salivary glue protein Sgs-3 precursor.
 DE Name=Sgs3;
 GN Drosophila simulans (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7240;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=88332966; Pubmed=3138416;
 RX Martin C.H., Mayeda C.A., Meyerowitz E.M.;
 RT "Evolution and expression of the Sgs-3 glue gene of Drosophila."
 RL J. Mol. Biol. 201;273-287(1988).
 CC -1- DEVELOPMENTAL STAGE: Produced by third-instar larvae.
 DR PIR; S01358; S01358.
 DR FlyBase; FBgn0012853; Dslm\Sgs3.
 KW Repeat; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 217 Salivary glue protein Sgs-3.
 SQ SEQUENCE 217 AA; 22750 MW; D29894B340257881 CRC64;

Query Match 13.5%; Score 80.5; DB 1; Length 217;
 Best Local Similarity 29.1%; Pred. No. 16;
 Matches 30; Conservative 10; Mismatches 46; Indels 17; Gaps 5;

QY 11 PTLKSVPCSLVTSYLNT---EDLSLMLWPKPDHSGRTREVSHTVPSKRGTAASPCWPLAGAV 64
 DB 90 PTKCKSSTTTTTRAPPTTCTKSTTTTTHHKPFTTSHSTPKTKKHTTTPKTKKHTTTPK 149

QY 65 CWPLAGAVPSPVSRLEALTRAVQVAEPLG--SCGFGGCPG 105
 DB 150 TKPKKHTTPTTTT-----TTPKCGCKSGGPGGPKG 183

RESULT 10;
 ID HXA9_MORSA STANDARD; PRT; 269 AA.
 AC Q9PMD5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Homeobox protein Hox-A9.
 DR Name=HoxA9;
 OS Morone saxatilis (Striped bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthopterygii; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Moronidae; Morone.
 NX NCBI_TaxID=34816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=925259633; Pubmed=10327649;
 RA Snell E.A., Scemama J.L., Stollwag E.J.;
 RT "Genomic organization of the Hoxa4-Hoxa10 region from Morone saxatilis: Implications for Hox gene evolution among vertebrates."
 RL J. Exp. Zool. 285;41-49(1999).
 CC -1- FUNCTION: Sequence-specific transcription factor which is part of a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Belongs to the Abd-B homeobox family.
 CC -1- SIMILARITY: Contains 1 homeobox domain.

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CC -----
 DR EMBL; AF089743; AAD46396.1; -
 DR HSSP; P02833; 9ANT.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeodommain_Like.
 DR InterPro; IPR006711; Hox9 act.
 DR InterPro; IPR00047; HTH_Iamdrepressr.
 DR Pfam; PF00046; Homeobox; 1.
 DR Pfam; PF04617; Hox9 act; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; Hox; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 KW Developmental protein; DNA-binding; Homeobox; Nuclear protein;
 KW Transcription regulation.
 FT DNA_BIND 202 261 Homeobox.
 SQ SEQUENCE 269 AA; 29600 MW; 8D49DCB0597D2A4C CRC64;

Query Match 13.5%; Score 80.5; DB 1; Length 269;
 Best Local Similarity 37.3%; Pred. No. 21;
 Matches 28; Conservative 7; Mismatches 29; Indels 11; Gaps 4;

QY 12 TLKSVPCSLVTSYLNTEDLSLMLWPK-PDL-HSGTRREVSHTVPSKRGTAAS 63
 DB 6 TLTSYV---VDSLILPESSELSVPRRYSGRGLQARQASASISPHSSEIGCTCFPSKDPVFG 62

QY 64 PCWPLAGAVPSPVSR 78
 DB 63 PSMWVDAQPPGTVS 77

RESULT 11

Q9PE02
 ID Q9PE02 PRELIMINARY; PRT; 690 AA.
 AC Q9PE02;
 DT 01-OCT-2002 (TRMBLrel. 22, Created)
 DT 01-OCT-2002 (TRMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Hypothetical protein XCC0181.
 GN OrderedListNames=XCC0181;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Cláudia L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dowry H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Kasuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madela A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Midanin J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,
 RA Spínola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kikajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL: AE012114; AAA39500.1; -
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR008941; TPR-like.
 DR Pfam: PF00515; TPR; 6.
 DR SMART: SM00028; TPR; 5.
 DR PROSITE: PSS0005; TPR; 1.
 DR PROSITE: PSS0293; TPR_REGION; 1.
 DR Complete proteome; Hypothetical protein; Repeat; TPR repeat.
 KW SEQUENCE 690 AA; 75528 MW; 733A01F0DEDBACC3 CRC64;
 SQ
 Query Match 13.0%; Score 79.5; DB 2; Length 690;
 Best Local Similarity 28.6%; Pred. No. 70;
 Matches 28; Conservative 8; Mismatches 39; Indels 23; Gaps 4;
 QY 19 SLVTSLYLPTNEDLSLWLM-----PKPDHSGT---RTEVSTHTVPSKRGTAAPC--W 66
 Db 395 SLLESLPAPQQTIVLRPMVGNVQDRAGQPDAAALATWMOFHEHQHRLRPLPPOAKKPFMOW 454
 QY 67 PLAGAVP-----SPTVSRLEALTRAUVQAEPL 93
 Db 455 PAVGSIPTVTSARPLFWGPPGSHVERLIAMVDAATPL 492
 RESULT 12
 Q93Q78 PRELIMINARY; PRT; 536 AA.
 AC Q93Q78;
 DT 01-DEC-2001 (TRMBLrel. 19, Created)
 DT 01-DEC-2001 (TRMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Benzoate dioxygenase reductase.
 GN Name=dogZ;
 OS Rhodococcus sp. 19070.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.
 NCBI_TaxID=161384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=19070;
 SQ

RX MEDLINE=21268842; PubMed=113715157;
 RA Haddad S., Eby D.M., Neidie E.L.;
 RT "Cloning and expression of the benzoate dioxygenase genes from
 RT Rhodococcus sp. strain 19070.";
 RL Appl. Environ. Microbiol. 67:2507-2514(2001).
 DR EMBL: AF279141; AAK58905.1; -
 DR HSP; P07771; ICRH.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR006058; 2FE2S_ID_BS.
 DR InterPro: IPR008990; E_transp_acc.
 DR InterPro: IPR008333; FAD_binding_6.
 DR InterPro: IPR001041; Ferredoxin.
 DR InterPro: IPR001709; FPN_cyt_reductase.
 DR InterPro: IPR001433; Oxid_FAD/NAD(P).
 DR InterPro: IPR001221; Phe_hydroxylase.
 DR Pfam: PF00970; FAD_binding_6; 1.
 DR Pfam: PF00111; Fer2; 1.
 DR Pfam: PF00175; NAD_binding_1; 1.
 DR PRINTS: PR00371; FENCR.
 DR PRINTS: PR00410; PHEHYDRIASE.
 DR PROSITE: PS00197; 2FE2S_FERRDOXIN; 1.
 KW 2Fe-2S; Dioxygenase; Iron; Iron-sulfur.
 SQ SEQUENCE 536 AA; 58643 MW; 97ED577853B5982D CRC64;
 Query Match 13.0%; Score 77.5; DB 2; Length 536;
 Best Local Similarity 25.7%; Pred. No. 82;
 Matches 27; Conservative 10; Mismatches 35; Indels 33; Gaps 4;
 QY 10 LPTLTKSVFC-----SLVTSLYLP---NTEDLSLWLMKPKPDHSGTSTREVTHTV 55
 Db 262 LPWFTDYCVSDSESTAPKNGYVTGLFPERKHLNDGVDVLYLGGPRVWAVRTHLDEGI 321
 QY 56 -----PSKRGTAAPCPLAGAVPSPVSRLEALTRAUQ 88
 Db 322 SVTNFYFEKFNNSGATPGAAEP-----APRPEREIEAATRAAE 359
 RESULT 13
 Q9P8U3 PRELIMINARY; PRT; 554 AA.
 AC Q9P8U3;
 DT 01-OCT-2000 (TRMBLrel. 15, Created)
 DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)
 DE Beta (1-3) glucanoseyltransferase Gel3p (Fragment).
 GN Name=GEL3;
 OS Aspergillus fumigatus (Sartoria fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 NCBI_TaxID=5085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS 144. 89;
 RX MEDLINE=20233679; PubMed=10769178;
 RA Mounya I., Monod M., Fontaine T., Hennissat B., Lechenne B.,
 RA Latge J.P.;
 RT "Identification of the catalytic residues of the first family of
 RT beta(1-3)glucanoseyltransferases identified in fungi.";
 RL Biochem. J. 347:741-747(2000).
 DR EMBL: AF208040; AAF40140.1; -
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR InterPro: IPR004886; GAST1.
 DR Pfam: PF03198; GAST1; 1.
 DR Transferase.
 KW NON TER 554 554
 FT SEQUENCE 554 AA; 58097 MW; 57D0236A74D44ADA CRC64;
 SQ
 Query Match 12.9%; Score 77; DB 2; Length 554;
 Best Local Similarity 25.0%; Pred. No. 94;
 Matches 34; Conservative 17; Mismatches 51; Indels 34; Gaps 6;

QY 7 LLLPPTLKSVFCSLVTSYLPTNTEDLSL-----WLMKPKD-----LHSGRTREVSTH 53
 DB 281 VLFPGMDVWVSGSIIYMTFETINDYGLVSVSGSAVTPPEDFYLSSEI0SATPTGVNSA 340
 QY 54 TV-----PSKPGTASPWCWPLAGAVPSP-----TVSRLEALTRAVQVABPLGSG--- 95
 DB 341 SYSPPTNSPAPCPVVDPTW-LAKSSPLPPTPMALGSCWMSYLSGCVVKDSDVDAKCYGELRG 399
 QY 96 --CGFQGGPCPRRRD 109
 DB 400 QVCGYGGGICDGIARN 415

RESULT 14

Q8XSC3 PRELIMINARY; PRT; 401 AA.
 ID Q8XSC3
 AC Q8XSC3; 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE PROBABLE CHROMATE TRANSPORT TRANSMEMBRANE PROTEIN.
 GN Name=chrA; Synonyms=RS03924; OrderedLocustNames=RS00555;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OG Plasmid megaplasmid.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OC NCBI_TaxID=305;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Broctier P., Camus J.C., Catolico L.,
 RA Chandel M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
 RA Weisenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646079; CAD17706.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0015109; P:chromate transporter activity; IEA.
 DR GO; GO:0015703; P:chromate transport; IEA.
 DR InterPro; IPR003370; Chromate_transpt.
 DR Pfam; PF02417; Chromate_transp; 2.
 DR TIGRFAMs; TIGR00937; 2A51; 1.
 KW Complete proteome; Plasmid; Transmembrane.
 SQ SEQUENCE 401 AA; 42639 MW; E6B5C13BBD66CB6C CRC64;

Query Match 12.9%; Score 76.5; DB 2; Length 401;
 Best Local Similarity 34.3%; Pred. No. 74;
 Matches 24; Conservative 8; Mismatches 33; Indels 5; Gaps 3;

QY 2 LMWLVLLPPTLKSVFCSLVTSYLPTNTEDLSLWLPKPD--LHSGRTREVSTHVPSPK 59
 DB 159 LMLVYLVVLAITYVTVTESEVAVMLPLAG--GVLVMLRAPPKMLRQSGSLNVAAPAPTRPAS 216
 QY 60 GTASPC-WPL 68
 DB 217 GILGIDWPL 226

RESULT 15

Q8NCU7 PRELIMINARY; PRT; 369 AA.
 ID Q8NCU7
 AC Q8NCU7; 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Guo J.H., Yu L.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF504646; AAM28197.1; -
 DR InterPro; IPR008973; C2_CatE.
 KW Hypothetical protein.
 SQ SEQUENCE 369 AA; 39755 MW; 469963F6069A3CF1 CRC64;

Query Match 12.8%; Score 76; DB 2; Length 369;
 Best Local Similarity 29.2%; Pred. No. 76;
 Matches 31; Conservative 13; Mismatches 50; Indels 12; Gaps 3;

QY 8 LLLPPTLKSV-----FCSLVTSYLPTNTEDLSLW--LMPKPDLS-----GRTREVSTH 55
 DB 91 LSLPFLPRVRYTAYGFCALLSEPHTRKESLLLGPPAPRAHYVGGGGPPDALLGTLRV 150
 QY 56 PSKPGTASPWCWPLAGAVPSPPTVSRLEALTRAVQVABPLGSGCGFQGG 101
 DB 151 PPAFGPTAPAGCPRPPQDALARRRRCGRLLRVDPGLSRALRAG 196

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 Job time : 96 secs

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OM protein - protein search, using sw model

Run on: December 25, 2004, 16:13:47 ; Search time 23 Seconds
(without alignments)
314.290 Million cell updates/sec

Title: US-10-063-728-114
Perfect score: 595
Sequence: 1 MMWLVLLLPRLKSVFCSL.....APPLGSGGFGGPGRRRD 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCUTUS COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfill1seq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	15.5	381	3	US-09-257-580-2
2	81.5	13.7	654	4	US-09-252-991A-18441
3	75	12.6	134	4	US-09-252-991A-25639
4	74.5	12.5	555	3	US-08-581-148C-16
5	73.5	12.4	124	4	US-09-489-039A-14266
6	73.5	12.4	246	4	US-09-252-991A-25102
7	72.5	12.2	141	4	US-09-252-991A-25082
8	72.5	12.2	220	4	US-09-252-991A-25865
9	71.5	12.0	297	4	US-09-252-991A-28842
10	71.5	12.0	369	4	US-09-252-991A-22549
11	71.5	12.0	475	4	US-09-252-991A-19177
12	70	11.8	207	4	US-09-252-991A-30613
13	70	11.8	1271	1	US-08-095-734-2
14	70	11.8	1271	2	US-08-444-623-2
15	70	11.8	1271	3	US-08-471-869-2
16	70	11.8	1271	3	US-09-342-563-2
17	70	11.8	1271	5	PCUT-US94-08267-2
18	69.5	11.7	109	4	US-09-800-729-184
19	69.5	11.7	370	4	US-09-252-991A-18438
20	69	11.6	250	4	US-09-252-991A-16664
21	68.5	11.5	295	4	US-09-489-039A-7975
22	68.5	11.5	321	4	US-09-252-991A-23173
23	68.5	11.5	446	2	US-08-822-171-3
24	68.5	11.5	472	2	US-08-822-171-2
25	68.5	11.5	1239	1	US-08-026-138E-3
26	68	11.4	438	4	US-09-252-991A-29390
27	68	11.4	703	3	US-09-167-206-5

28	67.5	11.3	119	4	US-09-252-991A-28425	Sequence 28425, A
29	67.5	11.3	191	4	US-09-252-991A-24024	Sequence 24024, A
30	67.5	11.3	203	4	US-09-252-991A-21469	Sequence 21469, A
31	67.5	11.3	208	4	US-09-252-991A-19982	Sequence 19982, A
32	67.5	11.3	224	3	US-09-199-637A-305	Sequence 305, App
33	67.5	11.3	522	3	US-09-075-272-3	Sequence 2, Appl1
34	67.5	11.3	622	3	US-09-075-272-2	Sequence 3, Appl1
35	67.5	11.3	673	4	US-09-252-991A-29503	Sequence 29503, A
36	67.5	11.3	179	4	US-09-252-991A-18755	Sequence 18755, A
37	67	11.3	661	4	US-09-252-991A-32899	Sequence 32899, A
38	67	11.3	830	4	US-09-252-991A-22004	Sequence 22004, A
39	67	11.3	967	3	US-09-313-677-17	Sequence 17, Appl1
40	67	11.3	976	3	US-08-894-997-50	Sequence 50, Appl1
41	67	11.3	1428	4	US-09-644-827B-7	Sequence 7, Appl1
42	67	11.3	2629	2	US-08-751-189-4	Sequence 4, Appl1
43	67	11.3	2629	2	US-09-060-83E-4	Sequence 4, Appl1
44	67	11.3	2629	3	US-09-184-44E-4	Sequence 4, Appl1
45	66.5	11.2	143	4	US-09-252-991A-17919	Sequence 17919, A

ALIGNMENTS

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RESULT 1
US-09-257-580-2      Application US/09257580
; Sequence 2, Appl1
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/1257,580
; PRIOR FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
; US-09-257-580-2

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Query Match      15.5%; Score 92; DB 3; Length 381;
Best Local Similarity 38.6%; Pred. No. 0.053;
Matches 27; Conservative 6; Mismatches 27; Indels 10; Gaps 4;
QY 9 LRP---TLKSVFCSLVTSLYLPNTEDLSLWPKPDLHSGTRTEVSTHTVPSKPGTASPC 65
Db 25 LRPENNVLSSSELCPPAVDELLP--SSVNWU-----DESDDAPRMPTATSPAPAPGA-PS 77
QY 66 WPLAGAVPSP 75
Db 78 WPLSSVSPSP 87
RESULT 2
US-09-252-991A-18441
; Sequence 18441, Appl1
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18441

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LENGTH: 654
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18441

Query Match 13.7%; Score 81.5; DB 4; Length 654;
 Best Local Similarity 26.4%; Pred. No. 1.6;
 Matches 33; Conservative 8; Mismatches 41; Indels 43; Gaps 6;

QY 27 PNTEDLSLW-----LMPKPDHSGTRT-----EVSHTHTVP-SKRGTAAPC----- 65
 Db 4 PPTRSMPWPACTAATAATPSPPTSSSIRAFPRPGPAATSPITKATPASHSPPCASPS 63
 QY 66 ---WPLAGAVSPPTVSR--LEALTRAVQVAEP-----LGGCGFGGSPC 103
 Db 64 SPTWKTSPAPSPFANGWMTSAWTAARCSAHNENGRKRGRRSSRSGAAGAFSGFAA 123
 QY 104 PGRRR 108
 Db 124 PSRRR 128

RESULT 3
 US-09-252-991A-25639
 Sequence 25639, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 PRIOR FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 25639
 LENGTH: 134
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25639

Query Match 12.6%; Score 75; DB 4; Length 134;
 Best Local Similarity 27.2%; Pred. No. 1;
 Matches 34; Conservative 10; Mismatches 43; Indels 38; Gaps 7;

QY 2 LHWLVLLLLPTLKSVCGLVTSYLTPNTEEDLSLWMPKPDHSGTRTEVST---HTVPSK 58
 Db 26 VWM-----KPTVSTAWTMS--TSSRAPST-----WPTT---SGCCRRPSSWCASITPPGR 68
 QY 59 PGTAPCPWPLAGAV-----PSPTVSRLEALTRAVQVAEPPIGSGCGFGGSPC 103
 Db 69 ASISSSSMWPSPFICTTACTCICRPWKAATSSRSRSTTRR---ATACGSRRRRPAARA 125
 QY 104 PGRRR 108
 Db 126 PGRRR 130

RESULT 4
 US-08-581-148C-16
 Sequence 16, Application US/08581148C
 Patent No. 6060644
 GENERAL INFORMATION:
 APPLICANT: Schnable, Patrick S.
 APPLICANT: Robertson, Donald S.
 APPLICANT: Hansen, Joel D.
 APPLICANT: Nikolau, Basil J.
 APPLICANT: Xu, Xiaojie
 APPLICANT: Xia, Yiji
 TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID

TITLE OF INVENTION: GENES
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Volt & Meyer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/581,148C
 FILING DATE: 29-DEC-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Larcher, Carol
 REGISTRATION/DOCKET NUMBER: 71380
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 616-5600
 TELEFAX: (312) 616-5700
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 555 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-581-148C-16

Query Match 12.5%; Score 74.5; DB 3; Length 555;
 Best Local Similarity 30.9%; Pred. No. 7.5;
 Matches 30; Conservative 10; Mismatches 44; Indels 13; Gaps 6;

QY 3 W-WLVLLLLPTLKSVCGLVTSYLTPNTEEDLSLWMPKPDHSGTRTEVSTHTVPSKPGT 61
 Db 25 MWDMMNVIMQTL--IAAVLVTSRVFPATSDLSAM-----DLR-GWAAVAVLVAAVSEPAF 76
 QY 62 ASPCPWPLAGAVSPPTVSRLEALTRAVQVAEPPIGSGCGF 98
 Db 77 ---YMAHRAHLHGLPFRSRYSHLSHSPQATQAL-TAGF 109

RESULT 5
 US-09-489-039A-14266
 Sequence 14266, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 PRIOR FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 14266
 LENGTH: 124
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-14266

Query Match 12.4%; Score 73.5; DB 4; Length 124;
 Best Local Similarity 30.7%; Pred. No. 1.4;
 Matches 23; Conservative 6; Mismatches 35; Indels 11; Gaps 3;

QY 38 PKPDHSGTRTEVSTHTVPSKRGTAAPCWPPLAGAV-----PSPTVSRLEALTRAVQV 89
 Db 15 PGP SARAGSEKASPPAAPA-GSAHPA--AAGAVGSSAPGRWPAARRRRSGSPVAVPA 71

QY 90 AEPGSCGFGGBCP 104
 DB 72 ALPAGTACTAPCP 86

RESULT 6
 US-09-252-991A-25102
 ; Sequence 25102, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25102
 ; LENGTH: 246
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25102

Query Match 12.4%; Score 73.5; DB 4; Length 246;
 Best Local Similarity 28.6%; Pred. No. 3.4;
 Matches 26; Conservative 10; Mismatches 34; Indels 21; Gaps 5;

QY 35 WMPKEDLHSGTRTEVSTHTVPSKPGTASPCWPLAGAVSPPTVSRLEALTRAVQVAE-P-92
 DB 34 WMPKEDLHSGTRTEVSTHTVPSKPGTASPCWPLAGAVSPPTVSRLEALTRAVQVAE-P-92

QY 77 VSRLEALTRAVQVAEPLGSCGFGGBCPGR 107
 DB 94 -TRSSASWSPCCGRSSTGTCRS--CPARR 121

RESULT 7
 US-09-252-991A-25082
 ; Sequence 25082, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25082
 ; LENGTH: 141
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25082

Query Match 12.2%; Score 72.5; DB 4; Length 141;
 Best Local Similarity 30.3%; Pred. No. 2.1;
 Matches 23; Conservative 6; Mismatches 34; Indels 13; Gaps 3;

QY 34 WMPKEDLHSGTRTEVSTHTVPSKPGTASPCWPLAGAVSPPTVSRLEALTRAVQVAE-P-92
 DB 9 LMRFRPFRRRRPPGR-----ADPGAAATGW--GMPDIFVPAARVRRGGSGAMRIP 56

QY 93 LGSFCGFGGBCPGR 108

DB 57 RRLETEGWRCPCWRRR 72

RESULT 8
 US-09-252-991A-25865
 ; Sequence 25865, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25865
 ; LENGTH: 220
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25865

Query Match 12.2%; Score 72.5; DB 4; Length 220;
 Best Local Similarity 35.8%; Pred. No. 3.8;
 Matches 24; Conservative 5; Mismatches 29; Indels 9; Gaps 2;

QY 40 PDLHSGTRTEVSTHTVPSKPGTASPCWPLAGAVSPPTVSRLEALTRAVQVAEPLGSCGFGQ 99
 DB 142 PARHGRRTTTPVARRRPAAPATASRSAAATGPPGQVAVQVRRARR-----PAGSAGWR 195

QY 100 GGPCCGR 106
 DB 196 S---PGR 199

RESULT 9
 US-09-252-991A-28842
 ; Sequence 28842, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 28842
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-28842

Query Match 12.0%; Score 71.5; DB 4; Length 297;
 Best Local Similarity 28.4%; Pred. No. 7.2;
 Matches 19; Conservative 6; Mismatches 31; Indels 11; Gaps 2;

QY 35 WMPKEDLHSGTRTEVSTHTVPSKPGTASPCWPLAGAVSPPTVSRLEALTRAVQVAEPLGSCGFGQ 99
 DB 227 WRMSR--CHSSSTVVPASCMRSSPSTCCRAVAVHGMPTSTPSASBSTSSAPCWTP 284

QY 86 AVQVAEP 92
 DB 285 ATWGCPR 291

Query Match 11.8%; Score 70; DB 1; Length 1271; Best Local Similarity 23.7%; Pred. No. 70; Matches 37; Conservative 10; Mismatches 59; Indels 50; Gaps 7;

QY 2 LWWL-----VLLLLPTLKVFCSLVTSLYLP-NTEDLSLWMPKPDHSG 45
Db 1060 IWWLARGLEFPQDGEFGELLPFNPTGAFQFLLYVVVDLPHIAQIATWMLGQYPLL5A 1119
QY 46 TRTEVSTH-----TVPSK--PGTASPCWPLAGAVPS----- 74
Db 1120 ALTGVAHGHGATGTLGSLGSLAIPSAALPVAVVPBELTPVAAAPMLAVAGVPAVAAPGM 1179
QY 75 -PTVSRLEALTRAVQVAEPL-GSCGFGGFC-PGRR 107
Db 1180 LPASAPAPAAAAGATVAGTTPPATGFGGLPALPGRR 1215

RESULT 14

US-08-444-623-2
; Sequence 2, Application US/08444623
; Patent No. 5866405
; GENERAL INFORMATION:
; APPLICANT: Aldovini, Anna
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: Homologously Recombinant Slow Growing
; TITLE OF INVENTION: Mycobacteria and Uses Therefor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,623
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/095,734
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: 07/711,334
; FILING DATE: 06-JUN-1991
; APPLICATION NUMBER: 07/367,894
; FILING DATE: 19-JUN-1989
; APPLICATION NUMBER: PCT/US90/03451
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: PCT/US89/02962
; FILING DATE: 07-JUL-1989
; APPLICATION NUMBER: 07/361,944
; FILING DATE: 05-JUN-1989
; APPLICATION NUMBER: 07/223,089
; FILING DATE: 22-JULY-1988
; APPLICATION NUMBER: 07/216,390
; FILING DATE: 07-JUL-1988
; APPLICATION NUMBER: 07/163,546
; FILING DATE: 03-MAR-1988
; APPLICATION NUMBER: PCT/US88/00614
; FILING DATE: 29-FEB-1988
; APPLICATION NUMBER: 07/020,451
; FILING DATE: 02-MAR-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH193-11M2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-623-2

Query Match 11.8%; Score 70; DB 2; Length 1271; Best Local Similarity 23.7%; Pred. No. 70; Matches 37; Conservative 10; Mismatches 59; Indels 50; Gaps 7;

QY 2 LWWL-----VLLLLPTLKVFCSLVTSLYLP-NTEDLSLWMPKPDHSG 45
Db 1060 IWWLARGLEFPQDGEFGELLPFNPTGAFQFLLYVVVDLPHIAQIATWMLGQYPLL5A 1119
QY 46 TRTEVSTH-----TVPSK--PGTASPCWPLAGAVPS----- 74
Db 1120 ALTGVAHGHGATGTLGSLGSLAIPSAALPVAVVPBELTPVAAAPMLAVAGVPAVAAPGM 1179
QY 75 -PTVSRLEALTRAVQVAEPL-GSCGFGGFC-PGRR 107
Db 1180 LPASAPAPAAAAGATVAGTTPPATGFGGLPALPGRR 1215

RESULT 15

US-08-471-869-2
; Sequence 2, Application US/08471869
; Patent No. 6022745
; GENERAL INFORMATION:
; APPLICANT: Aldovini, Anna
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: Homologously Recombinant Slow Growing
; TITLE OF INVENTION: Mycobacteria and Uses Therefor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,869
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08267
; FILING DATE: 22-JUL-1994
; APPLICATION NUMBER: US 08/095,734
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 07/711,334
; FILING DATE: 06-JUN-1991
; APPLICATION NUMBER: 07/367,894
; FILING DATE: 19-JUN-1989
; APPLICATION NUMBER: US 07/367,894
; APPLICATION NUMBER: PCT/US90/03451
; FILING DATE: 18-JUN-1990
; APPLICATION NUMBER: PCT/US89/02962
; FILING DATE: 07-JUL-1989
; APPLICATION NUMBER: 07/361,944

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? FILING DATE: 05-JUN-1989
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/223,089
? FILING DATE: 22-JUL-1988
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/216,390
? FILING DATE: 07-JUL-1988
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/163,546
? FILING DATE: 03-MAR-1988
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US88/00614
? FILING DATE: 29-FEB-1988
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/020,451
? FILING DATE: 02-MAR-1987
? ATTORNEY/AGENT INFORMATION:
? NAME: Granahan, Patricia
? REGISTRATION NUMBER: 32,227
? REFERENCE/DOCKET NUMBER: WHI93-11MA2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-861-6240
? TELEFAX: 617-861-9540
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1271 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-471-869-2

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? Query Match 11.8%; Score 70; DB 3; Length 1271;
? Best Local Similarity 23.7%; Pred. No. 70;
? Matches 37; Conservative 10; Mismatches 59; Indels 50; Gaps 7;

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QY 2 LMWL-----VLLLLPTLKSVCSLVTSLYLP-NTEDLSLWIMPKPDLHSG 45
Db 1060 IMWLARGLEFPQDGEQFGCELLFTNPTGAFQFLLYVVVVVDLPTHTAQIATWMLGQYPOLLSA 1119
QY 46 TRTEVSTH-----TVPSK--PGTASPCWPLAGAVPS----- 74
Db 1120 ALTGVIHLGAIITGLAGISLSAIPSAIIPAVVPELTPVAAPMLAVAGVPAVAAPGM 1179
QY 75 -PTVSRLEALTRAVQVAEPL-GSCGFOGGPC-PGRR 107
Db 1180 LPASAPAPAAAAGATPAGTTPPAPGFCGLPALPGR 1215

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Search completed: December 25, 2004, 16:33:44
Job time : 24 secs

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